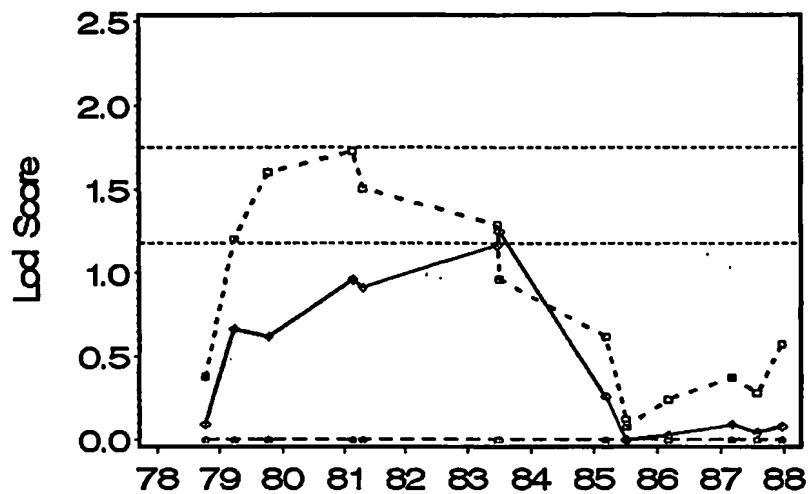


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A



B

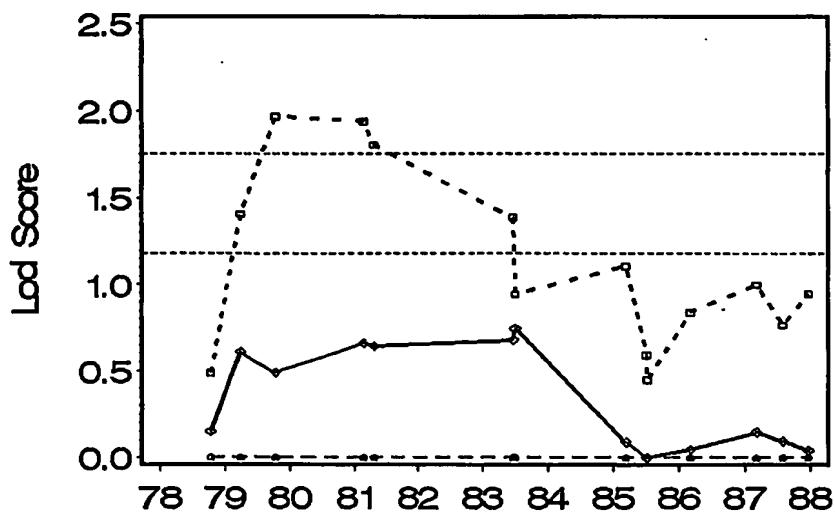


Fig. 1

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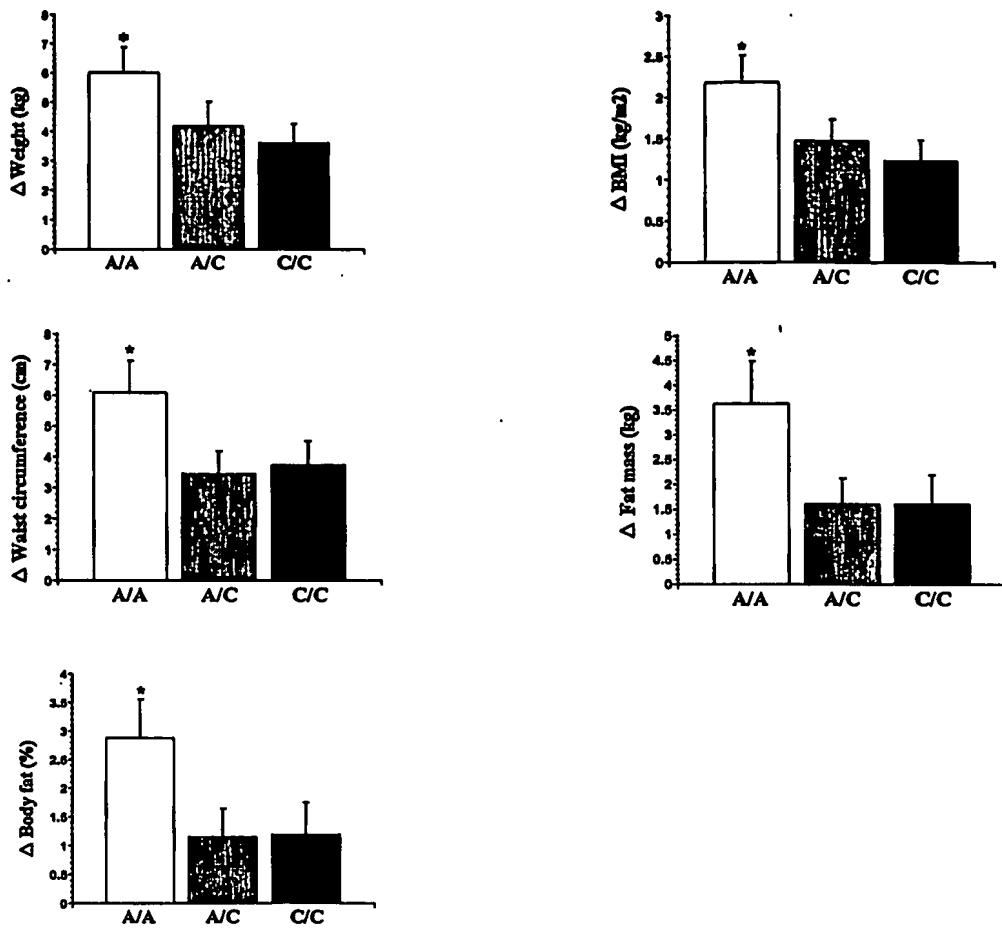


Fig. 2

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**Homo sapiens**MARRAGGARMFGSLLL**FALLAAGVAPLSWDLPEPRSRA**SKIRVHSRGNLWATGHFMOKKS 60**Mus musculus**MTRQAGSSWLLRGLLL**FALFASGVAPFNWDLPEPRSRA**SKIRVHPRGNLWATGHFMGKKS 60**Homo sapiens**LEPSSPSPLGTA**PHTSLRDQRLQLSHDLLGILLKKALGVSLSRPAPQI**QYRRLLVQILQK 121**Mus musculus**

LEPPSLSLVGTAPPNTPRDQRLQLSHDLLRILLRKKALGMNFSGPAPPIQYRRLLEPLLQK 121

Fig. 3

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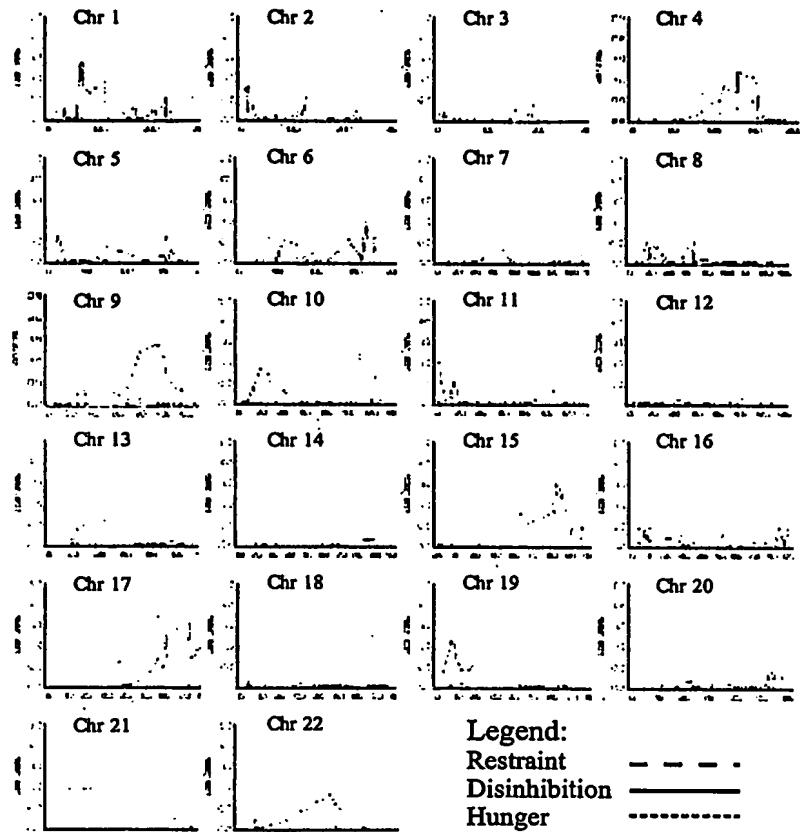


Fig. 4

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 NMB\_MUT  
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NMB\_REF  
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 NMB\_MUT  
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NMB\_REF  
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Fig. 5

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NMB_MUT		
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NMB_REF		
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NMB_MUT		
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NMB_REF		
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NMB_MUT		
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NMB_REF		
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NMB_MUT		
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NMB_MUT		
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NMB_MUT		
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NMB_REF		
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NMB_MUT		
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Fig. 5 (cont')

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NMB\_REF  
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NMB\_MUT  
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NMB\_REF  
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NMB\_MUT  
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NMB\_REF  
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NMB\_REF  
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Fig. 5 (cont')

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NMB\_REF  
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NMB\_REF  
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Fig. 5 (cont')

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NMB_REF		
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NMB_REF		
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NMB_REF		
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NMB_MUT		
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NMB_MUT		
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NMB_REF		
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NMB_MUT		
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NMB_REF		
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NMB_MUT		
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NMB_REF		
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NMB_MUT		
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NMB_REF		
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Fig. 5 (cont')

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NMB\_REF  
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NMB\_MUT  
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NMB\_REF  
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NMB\_REF  
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Fig. 5 (cont')

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NMB\_MUT  
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Fig. 5 (cont:')

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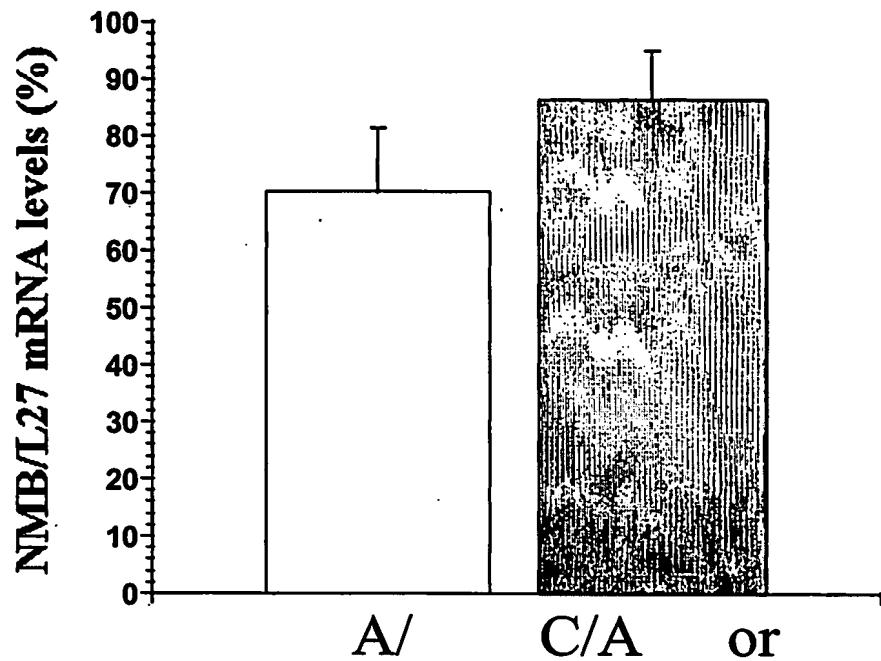


Fig. 6

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g-433 C&gt;T or rs1849288 (within NMB promoter)

NMB\_REF

CTGTTACCCGGAGGGAGAGCTCGCCGACCTCTACCCCTATGAAGAGAGGCTCAGAG

NMB\_MUT

CTGTTACCCGGAGGGAGAGCTCTCGCCGACCTCTACCCCTATGAAGAGAGGCTCAGAG

g.438 C&gt;G or IVS1+281 C&gt;G or rs2175567 (within NMB intron 1)

NMB\_REF

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NMB\_MUT

TTACCTTAGGCCAGACTTAACCGAATCTCTAACCGCTGGTGTGTTTGCTGCACCTCC

g.630 C&gt;A or IVS1+473 C&gt;A or rs2292462 (within NMB intron 1)

NMB\_REF

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NMB\_MUT

GGAAAAGCTGAGGGAGCAGGATTGCCACCACCCAGACACACCTTGTGGCTCCTGGTGAG

g.864 C&gt;A or c.217 C&gt;A (position on the coding sequence (cDNA) from the NMB first codon) or p.P73T (within NMB exon 2) or rs1051168

NMB\_REF

CCAGCCCCATCCCCATTGGGGACAGCTCCCCACACCTCCCTGAGGGACCAGCGACTGCAGC

NMB\_MUT

CCAGCCCCATCCCCATTGGGGACAGCTACCCACACCTCCCTGAGGGACCAGCGACTGCAGC

g.1043 G&gt;A or IVS2+66 G&gt;A (unknown in databases) (within NMB intron 2)

NMB\_REF

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NMB\_MUT

GGCCATCCCCGGATCCTGCATGGAAGGAATTACCACCCAGTACTGTATTAGGGTGTGACT

g.1173 G&gt;C or IVS2+196 G&gt;C(unknown in databases) (within NMB intron 2)

NMB\_REF

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NMB\_MUT

GCAAGAGCTCAAAGGAGGAACAGTCCAAACAAAGGAAGCTGACCTTCCCAGTAGACCCCAT

g.2493 A&gt;G or IVS2-251 A&gt;G or rs3809508 (within NMB intron 2)

NMB\_REF

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NMB\_MUT

GTGAGGGACGCTGACACTAGCCCAGCACCAGCAACTGTATTGGATTTCTCCACGATCT

Fig. 7

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g.2708 C>T or IVS2-36 C>T (unknown in databases) (within NMB intron 2)

NMB\_REF

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NMB\_MUT

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g.2817 T>C or g.\*38 T>C or rs3748371 (within NMB 3' untranslated region)

NMB\_REF

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NMB\_MUT

TAATGGGGCAGACACAACAGCGTGGCTTAGACTGTGCCACCCAGGGAAAGGTGCTGAATG

g.2863 C>G or g.\*84 C>G or rs1804012 (within NMB 3' untranslated region)

NMB\_REF

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NMB\_MUT

GTGCTGAATGGGACCCCTGTTGATGCCGCATCTGGATGTAAATCCTGAGCTCAAATCTCT

g.3022 C>A or g.\*243 C>A or rs3748372 (within NMB 3' untranslated region)

NMB\_REF

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NMB\_MUT

ATAAAAACCTTGCTTTACATAAAATGCCTGGCCTCTCCTTCACCCGTCTTTAGGGG

Fig. 7 (cont')